

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser	Ser
1				5					10	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met
1			5					10					15		
Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile
		20					25					30			
Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala
		35				40					45				
Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile
	50				55				60						
Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn
65				70				75				80			
Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala		
			85					90							

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Ser	Phe	Val	Thr	Thr	Gln	Pro	Glu	Ala	Leu	Ala	Ala	Ala	Ala	Ala
1			5					10				15			
Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala

50

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                20                25                30
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
   35                40                45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
   50                55                60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
   65                70                75                80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
                85                90                95
Ala Ala Gly

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(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

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Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Ala
 1                5                10                15
Asn Leu Gln Gly Ile Gly Thr Thr Met Asn Ala Gln Asn Ala Ala Ala
 20                25                30
Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser
 35                40                45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Met Tyr Gln Thr
 50                55                60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu
 65                70                75                80
Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
                85                90                95
Ala Ala Gly

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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Asp Pro His Ala Met Arg Asp Met Ala Gly Arg Phe Glu Val His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Arg Asp Met Ala Gly Arg Phe Glu Val His Ala Gln Thr Val Glu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Arg Phe Glu Val His Ala Gln Thr Val Glu Asp Glu Ala Arg Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ala Gln Thr Val Glu Asp Glu Ala Arg Arg Met Trp Ala Ser Ala

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Ala	Gly	Trp	Ser	Gly	Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Thr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Ala	Glu	Ala	Thr	Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser	Leu	Asp	Thr	Met	Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala	Gln	Met	Asn	Gln	Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala	Phe	Arg	Asn	Ile	Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Asn	Met	Leu	His	Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:47:

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gly	Val	Arg	Asp	Gly	Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu	Val	Arg	Asp	Ala	Asn	Asn	Tyr	Glu	Gln	Gln	Gln	Gln	Ala	Ser
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Asn	Asn	Tyr	Glu	Gln	Gln	Glu	Gln	Ala	Ser	Gln	Gln	Ile	Leu	Ser
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met	Ala	Ser	Arg	Phe	Met	Thr	Asp	Pro	His	Ala	Met	Arg	Asp	Met	Ala
1				5				10						15	
Gly															

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met	Thr	Ile	Asn	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met	Ile	Arg	Ala	Gln	Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

58

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Gln	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Ile	Val	Arg	Asp	Val	Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Leu	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids

59

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

She	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gly	Ser	Val	Ala	Cys	Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln	Glu	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu
1				5					10					15	
Gln	Ala														

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

60

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ile	Tyr	Glu	Gln	Ala	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid

61

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Gly	Asn	Asn	Met	Ala	Gln	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met	Ile	Arg	Ala	Leu	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met	Ile	Arg	Ala	Gln	Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Ser	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ala	Gly	Leu	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala	Glu	His	Gln	Ala	Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Ala	Glu	His	Gln	Ala	Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp
1			5						10					15

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ile	Ile	Ser	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ile	Ile	Arg	Asp	Val	Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Leu	Thr	Ala	Ser	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala	Ala	Cys	Gln
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Phe	Trp	Gly	Gly	Ala	Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly	Ser	Ala	Ala	Cys	Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Gln	Gly	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Val	Thr	Thr	Asn	Phe	Phe	Gly	Val	Asn	Thr	Ile	Pro	Ile	Ala	Leu	Asn
1			5					10					15		
Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile							
			20				25								

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Mycobacterium tuberculosis*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Asn	Glu	Ala	Asp	Tyr	Leu	Arg	Met	Trp	Ile	Gln	Ala	Ala	Thr	Val	Met
1			5					10					15		
Ser	His	Tyr	Gln	Ala	Val	Ala	His	Glu							
			20				25								

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 967 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

TGAGCGCCAA CCTACCGTC GTTTCGTAC ACGGACCGCA TGGCCTGCTC CCGGACTGCG    60
CGCTAGGGTC GCGGATCATT CCGGTAGCG GCGCTTTGGC CCACCGATAT GGGTTCCGTC    120
ACAGTGIGGT TCGCCGCGCG CCATCGGCG GATAACGCCA TGACCTCAGC TCGGCAGAAA    180
TGACAATGCT CCCAAGGCG TGAGCACCGG AAGACAACCTA AGCAGGAGAT CCGATGCCGT    240
TTGTGACTAC CCAACCAAA GCACTGGCGG CGGCGCGCGG CAGTCTGAG GGAATCGGCT    300
CGCATTSAA CGCCCAAAAT GCGGCTGCGG CCACTCCAC GACGGGGTG GTCCGGCGGC    360
CGCCGATGAA NTGTGCGCGC TGACGGCGGC TCAGTTGCGG GCACACGCGC AGATCTATCA    420
GGCCCTCAGC GCGCAGGCGG CCGCGATTCA CGAGATGTTT GTCAACACTC TACAGATGAG    480
CTCAGGGTCG TATGCTGCTA CCGAGGCGCG CAACCGCGCG GCGGCGCGGT AGAGGACTCA    540
CTGCGATGGA TTTTGGGGCG TTCCCGCGCG AGGTCAATTC GGTGCGGATG TATGCGGTTT    600
CTGGCTCGGC ACCAATGCTC GTTGGCGGCT CGGCTTGAAA CGGTTTGGCC GCGGAGCTGA    660
GTTCGGCGGC CACCGTTTAT GAGACGGTGA TCATTCAGCT CAGCAGTGAG CGGTGGCTAG    720
GTCCGCGCTC AGCGCGGATG GCGGAGGCG TTGCGCGCTA TGTGGCGTGG ATGACTGCGG    780
CTCGGCGGCA AGCGGAGCG GCGGCGACAC AGGCGAGGGC CGCCGCGCGC GCTTTTGAGG    840
CGGCGTTTTC CCGGACGGTG CCTCGCGGCT TGATCGCGCG CAACCGGCT TCGTTGATGC    900
AGCTGATCTC GACGAATGTC TTTGGTCTGA ACACCTCGCG GATCGCGCGC GCGGAAGCTC    960
AGTACGG

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Met Ser Phe Val Thr Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala
 1           5           10          15

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Thr Gln Pro Glu Ala Leu Ala Ala Ala Ala Asn Leu Gln Gly
 1           5           10          15

```

(2) INFORMATION FOR SEQ ID NO:86:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu	Ala	Ala	Ala	Ala	Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:87:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Ala	Asn	Leu	Gln	Gly	Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:88:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Ile	Gly	Thr	Thr	Met	Asn	Ala	Gln	Asn	Ala	Ala	Ala	Ala	Ala	Pro
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:89:

(1) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Asn Ala Gln Asn Ala Ala Ala Ala Pro Thr Thr Gly Val Val
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Thr Thr Gly Val Val Pro Ala Ala Ala Asp Gln Val Ser Ala Leu
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Pro Ala Ala Ala Asp Gln Val Ser Ala Leu Thr Ala Ala Gln Phe
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu	Val	Ser	Ala	Leu	Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Thr	Ala	Ala	Gln	Phe	Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Ala	Ala	His	Ala	Gln	Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met	Tyr	Gln	Thr	Val	Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Gln	Met	Phe
1				5				10						15	

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Ala	Gln	Ala	Ala	Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala	Ile	His	Glu	Met	Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe	Val	Asn	Thr	Leu	Val	Ala	Ser	Ser	Gly	Ser	Tyr	Ala	Ala	Thr
1			5					10					15	

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Ala Ser Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala Ala Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1784 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

ATCGTTCCT GCGGCAGCTA ATCCCCGGG ACATCGTCGC CGGCCASTAC GAGGTCAAAG      60
GCTGCATCGC GCACGGCGGA CTGGGCTGGA TCTACCTGCG TCTCGACCGC AATGTCAACG    120
GCCGTCCGCT GGTGCTCNAG GGCTGGTGC ATTCGGGTGA TGCCGAAGCG CAGGCAATGG    180
CGATGGCGGA AGCCAGTTC CTGGCGGAGG TGGTGCACCG GTCCATCGTG CAGATCTTCA    240
ACTTTGTGGA GCACACCGAC AGGCACGGGG ATCCGGTCCG CTACATCGTG ATGGAAATACG    300
TCGGCGGGCA ATCGCTCAAA CCGAGCAAGG CTCANAACT GCGCGTCGCG GAGGCCATCG    360
CCTACCTGCT GGAGATCCTG CCGGCGCTGA GCTACCTGCA TTCCATCGGC TTGCTCTACA    420
ACGACCTGAA GCCGGAARAC ATCATGCTGA CCGAGGAACA GCTCAAGCTG ATCGACCTGG    480
GCCCGGTATC GCGGATCAAC TCGTTCGGCT ACGTCTACCG GACCCAGGCG TTCCAGGCGC    540
CCGAGATCGT GCGGACCGGT CCGACGCTGG CCACCGACAT CTACACCGTG GGACGCACGC    600
TCCCGCGGCT CAGGCTGGAC CTGCCCACCC GCATGSCCGG TTATGTGGAT GGGCTACCCG    660
AAGACGACCC GTGCTGAAA ACCTAGGACT CTTACGGCCG GTTGCTGCGC AGGGCCATCG    720
ACCCCGATCC GCGGCAACCG TTCACCACCG CCGAAGAGAT GTCCGCGGCA TTGACGGGCG    780
TGTTGCGGGA GTGGGTGCGC CAGACACCGG GGTGCCCGCG CCAGGCTATC AACGATCTTC    840
AGTCCAGTTC GTTCGACATT TCGAGTGGAC TGCTGGTGGC GCACACCGAC GTGTATCTTG    900
ACGGGCAAGT GCACGCGGAG AAGCTGACCG CCAACGAGAT CGTGACCGCG CTGTGGGTTC    960
CGCTGGTGA TCCGACCGAC GTCCGAGCTT CGGTCTTGCA GGCACCGGTG CTCTCCAGC    1020
CGGTGCAGAC CTTAGACTCG NTCCGCGCGG CCGGCCACCG TGCGCTGGAC GCGGACGGCG    1080
TCGATTNTCC GAGTCAGTGG AGCTGCCGCT AATGGAAGTC CGCGGCTGTC TGGATCTCGG    1140
CGATGTGGCC AAGGCCACCC GAAACTCGA CGATCTGGCC GAACGCGTTG GCTGGCGATG    1200
GCCATTGGTC TGGTACCGGG CCGTCGCGGA GCTGCTCACC GGGGACTATG ACTCGGCGAC    1260
CAAAATTTTC ACCGAGGTGC TGGATACCTT TCCCGGCGAG CTGGCGCCCA AGCTCGGCTT    1320
GGCGGCCACC GCGGAATAG CCGGCAACAC CGACGAACAC AAGTCTATC AGACGGTGTG    1380
GAGCAACAC GACGGGCTGA TCTCGGCGGC TTTCGGACTG GCGAGAGCCC GGTGGGCGGA    1440
AGGTGATCGG GTCGGCGCGG TCGGACGCT GAGCGAGGTA CCGCCACTT CTCGGCATTT    1500

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CACCAACGCCA	CGGCTEACCA	GCGCGGTGAC	TCTGTTGTCC	GGCCGGTCAA	CGAGTGAGT	1560
CACCAACGAA	CAGATCCCG	ACGCGCGCCG	AAGAGTGGAG	GGCTGCCCC	CGACCGAACC	1620
ACGCTGCTG	CAGATCCCG	CGCTGTTCT	GGTGGGCGG	CTGGACTGGC	TGAAGGACAA	1680
CAAGGCGAGC	ACCAACCACA	TCTCGGTTT	CCGTTTCACT	AGTCACGGGC	TGCGGCTGGG	1740
TGTCGAGGCG	TCACTGCGCA	GCTTGGCCCG	GGTACGTCCT	ACTC		1784

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

ACAARACACT	CGGYGCGKGC	CGMTCCGGCC	TGATCGTCGG	TGATCAGCYT	CGTGCCAAAY	60
TGGGCACAAG	GTGCGCGCTE	CCCAANGAGT	TCTTCGCCCC	GTGCGMGCM	KAAC TGKCCCT	120
ATGNTGGTGG	GGTGCGCTCC	CGCANAAACC	GGGAATTAA	ACCCATTTTA	ACUGGCGUAG	180
AAGTTTCCTA	CATYTACCCN	GGGMMCCAA	CCGGGCGGCC	NANAAMTCCG	TCTTGANTC	240
CGANCGGTTG	CGGCTGTTCC	CGGCACTGCT	GACCGGCAAG	GATATCCGC	AGCGGCGCTT	300
GGCCAACGGG	TGGGTGCAAC	TGGCTTACGG	TGCGCACCGG	GACGCCATCA	CGGCTCGGA	360
GTCCGACCAAG	GTACTCAATG	CTGGCGACCA	CACCAAGCCAG	CAGACCAAAC	TGGTGCACGC	420
CGATCTCCAG	GCGCGCGCGC	CGGTGGCAT	ACGGATTGGT	CGAALCCAAAT	CCGAAGGAAAT	480
TCATCACGGA	CGGTACGGA	AAACGATCGC	CCCAATGGGN	GGACHACCCN	AGCCAGGCGN	540
ATTNACCTTT	NAACAAGTTG	GNGTAGGTTG	TTTGATATCG	AKCAACCGAT	ACGGAAGGGM	600
CCGCGGAATG	GTAGACCAAC	ACCAGTGCCC	NCAMGTMTG	CACCAATTTG	GTATCGCCCC	660
GCAGATCGGT	GACCCCGCCA	AGGCTTCCCG	ATGCGGAGAT	GAGGGTGACC	AGCCYGGTTG	720
ACCTGTTGAT	CAGGTTNTCC	CAGTGCCACG	TCGGCAGCTG	GCCGGT		766

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGGCACGAGA	ATGTCGCTTG	TGCTTCGATA	GGCACTTGCG	TGTGGTGGCG	CTGCCAGCGG	60
GTGAGCCAGG	TGCGCTGGTC	CAGGCCATCG	GGCGGGCGCA	GGAGCGCGAT	GTTGGCCAGA	120
CUUGGTGTAC	GAGAACCGGA	CTGACGNAAG	TGTGGGCGCT	GACGGCGGCT	CAGTTGGCGG	180
CACACGCCCC	GATCIATCAG	GCGCTCAGCG	CCCAGGCGGC	GGCGATTCACT	GAGATGTTCC	240
TCAACACTCT	ACAGATNANC	TCAGGCTCGT	ATGCTGCTAC	CGAGGCGCGC	AACCGCGCGG	300
CGGCGCGCTA	GAGGAGTCAC	TGCGATGGAT	TTTGGGGCGT	TGCGGCGCGA	GATCAATTCG	360
GTGCGGATGT	ATGCCGGTTC	TGGCTCGGCA	CCAATGGTCC	CTGCGGCGTC	GGCTTGGAAC	420
GGGTTGGCCG	CGGAGCTGAG	TTGCGCGGCC	ACCGGTTATG	AGACGCTGAT	CACTCACTTC	480
AGCAGTGAGG	GTTGGCTAGG	TGCGGCTCA	GGGCGGATGG	CGGAGGCGAGT	TGGGCGGAT	540
GTGGCGTGGA	TGAGTGCCGC	TGCGGCGCA	GGCGAGCGGG	CGGCGACGCG	GGCCAGGGCC	600
GCGCGGCGCG	CTTTTGAGGC	GGGTTTGCC	GCGAGCGTGG	CTCGGCGGTT	GATCGCGGCT	660

AACCGGSCCTT	CCTTGATGCA	GCTGATCTCG	ACGAAATGCTT	TTGGTCAGAA	CACCTCGGCG	720
ATCGCGGCGG	CCGAAGCTCA	GTACGGCGAG	ATGTGGGCCC	AAGACTCCGC	GGCGATGTAT	760
GCCTACGCGG	GCAGTTGCGC	GAGCGCTTCG	GCGGTCACGC	CGTTTAGCAC	GCAGCGGACG	800
ATTGCCAACC	CGACCGCTCA	GGGTACGCGG	GCGCGCGCGG	TGGCCACCGC	CGCGGTTACC	840
GCCCACTCGA	CGCTGACGGA	GATGATCACT	GCGCTACCCA	ACGCGCTGCA	AAGCCTCACC	880
TCACATCTGT	TGCAGTCGTC	TAACGGTCCG	CTGTCGTGGC	TGTGGCAGAT	CTTGTTTGGC	920
ACGCCCAATT	TCCCCAGCTC	AATTTGCGCA	CTGCTGACCG	ACCTGCAGCC	CTACGCGAGC	960
TTNTTNTATA	ACACCGAGGG	CTTGGCGTAC	TTCAAGCATCG	GCATGGGCAA	CAACTTCATT	1000
CAGTCGSCCA	AGACCTTGGG	ATTGATCGGC	TAGGCGGCGC	CGGCTGCGGT	CGCGGTTGCT	1040
GGGGATNCCG	CCAGGGGCTT	GCCTCGTCCC	G			1080

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2041 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGGCACGAGC	TCGTGCGGAT	CAGTGCCATT	GACGGCTTGT	ACGACCTTCT	GGGGATTGGA	60
ATACCCAAAC	AAGGGGGTAT	CTTTTACTCC	TCCTAGAGT	ACTTCGAAAA	AGGCTTGGAG	120
GAGCTGGCAG	CAGCGTTTCC	GGGTGATGGC	TGGTTAGGTT	CGGCGCGCGA	CAAATACGCC	180
GGCAAAAACC	GCAACCACTT	GAATTTTTC	CAGGAATCTG	CAGACCTCGA	TGTCAGCTC	240
ATCAGCCTGA	TCTACGACCA	GGCCACGCGG	GTGCGACGCA	CCGCGGACAT	CCTGGAGGCG	300
GGCAAGAAAG	GTCTGAGTT	CGTGGCGCGG	GTGGCTGTGG	ACCTGACCTA	CATCCCGGTC	360
GTGGGGCAGC	CCCTATCGGC	CGCCTTCCAN	GGCGCGTTTT	GGCGGGGGCG	GATGGCGGTA	420
GTGGGGCGCG	CGCTGCGCTA	CTTGGTGGTG	AAAACGCTGA	TCAACGCGAC	TCAACTCCTC	480
AAATTGCTTG	CCAAATTGGC	GGAGTTGGTC	GCGGCGCGCA	TTGCGGACAT	CATTTGCGAT	540
GTGGCGGACA	TCATCAAGGG	CATCCTCGGA	GAAGTGTGGG	ASTTCATCAC	AAACGGGCTC	600
AACGGCCTGA	AAGAGCTTTG	GGACAAGCTC	ACGGGGTGGG	TGACCGGACT	GTCTCTCTGA	660
GGGTGTGCGA	ACCTGGAGTC	CTTCTTTGCG	GGGCTCCCGG	GCCTGACCGG	CGGAGCTAGC	720
GGCTTGTGCG	AAGTGACTGG	CTTGTTCGGT	GGGCGCGGTC	TGTCCGCTAT	GTGCGGCTTC	780
GCTCAGCGCG	ATAGCCTGGC	GAGCTCAGCC	AGCTTGCGCG	CCCTGGCGCG	CATTGGGGGG	840
GGGTCCGGTT	TTGGGGGCTT	GCCGAGCCTG	GCTCAGGTCC	ATGCCGCTC	AACCTGGGCG	900
GCCTACGCGC	CCCGAGCTGA	TGGCGCGGTC	GGCGCGGCTG	CCGAGCAGGT	CGGCGGGGCG	960
TCCCACTGGG	TCTCGCGGCA	GGTTTCCCAA	CGTATGGGCG	GACCCGTAGG	CATGGCGGCG	1020
ATGCACCCCT	CTTCGGGGGC	GTGGAAGGCG	ACGACGACGA	AGAAGTACTC	GGAAGGGGCG	1080
GCGGCGGGCA	CTGAAGACGC	CGAGCGGCGG	CCAGTCGAAG	CTGACCGCGG	CGGTGGGCAA	1140
AAGGTGCTGG	TACGAAACGT	CGTCTAAGCG	CATGGCGAGC	CAATTCATT	GCTAGCCAGC	1200
GCCTAACAA	GGCAATGCT	AAACGGAAGG	GACACGATCA	ATGACCGAAA	ACTTGACCGT	1260
CCAGCGCGAG	CTCTCGGTC	TACTGGGCTC	GCACCATGAC	AACGCGCGCG	TGGATGCTTC	1320
CTCGGGGCTC	GAGCTGCGG	CTGGCCTAGG	CGAATCTGTG	GCGATCACTC	ACGCTCCGTA	1380
CTGCTCAGAG	TTCAACGACA	CGTTAAATGT	GTACTTGAAT	GCCACAAATG	CCCTGGGCTC	1440
GTCTTTGCAT	ACGCGCGGTC	TGATCTCGC	CAAAAGTCTT	CGAATTCGGG	CGAAGATATA	1500
TACCGAGGCG	GACGAAGCCT	GGCGCAAGGC	TATCGAAGCG	TTTCTTACCT	GACCACTTTT	1560
GCTGCGGCGA	GTGCAAGGCA	CGACGTAGCG	CAGGTGCTGT	CCCTCGTAGG	CGTGGATGCG	1620
ACCGGCGGAG	ACCAGCACCC	GCTGGGCAAC	GATGGGCAAG	GACAGTAGCT	CGCCCGGCTG	1680
CCCGGCTGCG	GTGGCGGCA	CAAAACCGGG	CAGTTGCGCC	TGGCGGAGCA	CGGTGGTGGG	1740
GGAGCCCAAC	GCGGCAAGCG	CGGTAACCA	TCCCGAGCCG	AGCAGGAGCG	AGAGGTCATG	1800
TTGCGCGGAT	CGGTTGCGGT	CAGCGATGAC	CTGCGCGGCG	CGCGGGGCGA	GTTCGTGCGG	1860
ATCGGGGCGC	GGGTGAGCCA	CAGTGGGCGA	GCTTAACTGA	GCGGCTGCGT	GGGGAGCGCG	1920

TGCTNCTGGA	TGAGATACTG	CGAGCATGCC	AGCAGCCAGC	GCATCCGACC	GGGTGAGGAA	1980
ATTGCTKGG	CGCCCTGCTG	GCAGCTGCTG	CGAGCTGTCC	CATCCCATCC	ACCTCTGTCT	2040
G						2041

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAGCTCACC	CTATCAACCA	ATACTTCTG	CACTCCAAGA	TCCAGGACAA	CTGGGGTTTT	60
ACCGAGCTGG	CGGCCACAC	CCGCCCGGAG	TCUTTCBAAG	AAATGCGGCA	CGCCGAGGAA	120
ATCACGATC	GCATCTTST	GCTGGAGGCT	TTSCGGAAT	ACCAAGCGAT	CGGTTCGTTG	180
CGTATCGGCT	AGACGCTCCG	CGAGCAATTT	GAGGCGGATC	TGGCGATCGA	ATACGAGCTG	240
TTGAATCCTC	TCAAGCCAGG	AAATGCTCAT	TCCCGGAGAA	AACAGGACAC	CACGAGGCTC	300
GTACTGCTGG	AGAAATCGT	TGCCGACGAG	GAAGAACACA	TGACTACTTT	GGAAACGACG	360
CTGGAGCTGA	TGGACAAGCT	AGGAGAGGAG	CTTTACTCGG	CGCAGTGGCT	CTCTCGGCTC	420
CCGACCTGAT	GGCCGCTTGA	GGATTCTCCG	ATACCACTCC	GGCCGCGGCT	GACAAGCTCT	480
AGCATGAGCT	CGAACAGGCA	TGGAGGCGCG	GATATGGCGG	GGCCGCGGCT	ACCGAGGACT	540
GGCCGCGGCT	CAATCGAGG	CGGTGGCGCG	CTGCTCAGTC	CGCTKXGACG	CAACATTATT	600
TTCAACGAC	TTGTGTTGG	GGTGTCTGTC	GCTGCGAGCG	GCCAAACCAT	CGTTGTGCTC	660
GCATTGCGCA	CGATCTCTGC	CGAGCTGGGC	AGCAACGTTG	ACCACTGCTG	GGCGGTCACC	720
AGCTATCTGC	TGGGGGGAAC	ACTSKYGEKE	ETGKKGKSKS	KRRMMKCTC	GGTGTCTGTC	780
TGGGGGGAAC	CAGGCTGCTG	CTAGGCTCCG	TGCTGCTCTT	CTCTGTTGTC	TCTGTCTGTC	840
GCGGTTTATC	GCAGACGATG	ACCATGCTGG	CGATCTCTCG	CGCACTGCAG	GGCGTGGGTC	900
CGGTTGCGAT	TTCCTTCACC	GGCTACGCGC	TGCGCGCTGA	GCTGGTCCCA	CTGCGGAGCC	960
GTGGCGGCTA	CCAGGGGCTC	TTAGTTCGCG	TGTTGCTGCT	CAACACGGTC	ACCGGTTCGC	1020
TGCTGGGGGG	CTGGCTCACC	GACTATCTGA	GCTGCGGCTG	GGCTTTCGCA	CCACGAGGCT	1080
CATCACGAC	CTGATCGCGG	TCATGCGGCG	GAACACGCGC	CTCGCGGCTG	TGCGGCGAGG	1140
TCCCTTGGGG	AACCTGCTCC	CACAGCGGCA	GAACGCTCGG	AAATGCGATG	GCCGAGCCAC	1200
AC						1202

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GGCGGCGGCA	GTTGGCCAGC	AGTTGGGGCG	GGGAGCGCGG	TTGGGAGACC	AAGAAATCGG	60
CTTGGGCAAG	CAGCGGGGAC	CGCGACCGCT	GATCAGTTTG	GATCGCGCGG	ACCGCGGCGG	120
ACCAATGCCA	TTCCGCGGCT	GAGGAAGTCG	GAANTNTGCG	CAGTGATGAC	GGCTGTCTGC	180
AACGCTTCCC	GGATTGCGCA	GCGGATCGGC	GCGAAGCGGC	GGTGTCTACC	ACCGGCGGAG	240
ACCTCTACNG	ACAGGCTCGC	ATAGCTGAAT	GAGCGCGGGT	AGCGGCGGCT	CGTTCGAGCG	300

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NGAATCCGGC CCGGAGACAA AAGATCCGTC GGCCTCCGGC CTCGGCCGACG ACAGCCACCT 360
TCACCCCGGC GTTATCCGTC GCGGCGATCG CATACCAGGC GCGGTCAAGG TNGCCGTTC 420
GGTAGTCACG CACCGACAAG GTGATYGGT CCATCCGCTN GACGCGCGGG GTGACGCTCG 480
GGCGGATCAM GTGCAC

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 849 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

TGGATTCCGA TAGCGTTTC GCGCCCTCGA CCGCCGACCA CGGCGCGCAG GCCTCCGAAC 60
GGGGGGCCCG GACGCTGGGA TTCGCGGGGA CCGCAACCA AGAAGCCCGG CTCGGGCGCG 120
TCGGGCTGAC CCGACTGGCC GTTGATGAGT TCGGCAACGG CCGCCGATG CCGATGTCG 180
CTGGGACCTG GAGCGAGGGC AGCAGCAGC CCGAGGCGCC CGACCGATCG GCGAGAGCGG 240
GAGCGGACCG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCAGT GGACCGGTAC 300
GGGTGGAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCGACAG TTGCTGCGCT 360
CCCATGTGGC GTTTCGCGCC AAGGCGGGGC TGATCGGCA CACGATCGCT CAGGCGGAGC 420
AGCGCGCAT GTGCGCTCAG GCGTTTCACC AGCGGGAGTC GTGCGCGCGG TTTCAGGCGG 480
CCCATGCGCG GTTTCGCGCG GCGCGCGCGA AAGTCAACAC CTTGTTGGAT CTCGCGCAGG 540
CGAATCTGGG TGAGGCGGCG GTTACCTATG TCGCGCGCGA TCGTGGCGCG GCGTGCAGCT 600
ATACCGGGTT CTGATCGAAC CCTGCTGACC GAGAGGACTT GTGATGTCGC AATCATGTA 660
CACTACCGCG GCGATGTTGG GTCAGCGCGG GATATGCGCC GATATGCGCG GCAGGCTGCA 720
GAGCTTGGCT GCGGAGATCG CCGTGAGCA GCGCGCGTTG CAGATGCGCT GCGAGGCGCA 780
TACCGGATC ACGTATCAGG CCGGCGAGGC ACANTGGTAA CCAGGCGCAG GAGATTTCG 840
TCCGCGCT

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1           5           10           15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
 20           25           30
Gln Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
 35           40           45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys
 50           55           60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
 65           70           75           80

```

Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
 85 90 95
 Phe

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Leu Val Ala Ser Gln Ser Ala Phe Ala Ala Lys Ala Gly Leu Met
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Ser	Ala	Phe	Ala	Ala	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gln	Ala	Glu	Gln	Ala	Ala	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly
1				5				10						15

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe	Gln	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Asn	Thr	Leu	Leu	Asp	Val	Ala	Gln	Ala	Asn	Leu	Gly	Glu	Ala	Ala
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid

81

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val Ala Ala
1 5 10 15
Asp Ala

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

CGGCACGAGA ATGTGCGCTG TGCCTGATA GCCACTTGGG TGTGGTCGGG CTGCCAGGCG 60
GTCAGCCAGG TGCCTTGGTC CAGGCCATCG GCGCGCGGCA GGAGCCCGAT GTTGGCCAGA 120
CCCGGTGTAC GAGAACCGGA CTCGACNAG TGTGCGCGCT GACGGCGGCT CAGTTCGCGG 180
CACACGCCCC GATCTATPCAG GCCGTACGG CCCAGGCCGC GGCATTCAC GAGATGTTGG 240
TCAACACTCT ACAGATNANC TCAGGGTCGT ATGCTGCTAC CAGAGCTCGC AACCGCGGCG 300
CGCCCGGCTA GAGGAGTCAC TCGGATGGAT TTTGGGGCGT TCCCGCCGGA GGTCAATTGG 360
GTGCGGATGT ATGCGGCTCC TGGCTCGGCA CCAATGGTCG CTGCGGCGTC GGCCTGGAAC 420
GGGTGGCCCG CGGAGCTGAG TTCGGCGGCC ACCGGTTATG AGACGGTGAT CACTCAGCTC 480
AGCAGTGAGG GTTGGCTAGG TCCCGCGTCA GCGCGGATGG CCGAGGCAGT TGCGCCGTAT 540
GTGGCGTGGA TGAGTGCCGC TCGCGCGCAA GCGGAGCAGG CGGCCACACA GGCAGGGGCC 600
GCCCGCGCCG CTTTGGAGGC GCGTTTGGC GCGAGCGTGC CTCGCGCGTT GATCGCGGCC 660
AACCGGCTT CTTGATGCA GCTGATCTCG ACAGATGCTT TTGGTCAGAA CACCTCGGCG 720
ATCGCGCGCG CCGAGCTCA GTACGGCGAG ATGTGCGGCC AAGACTCGCG GCGGATGTAT 780
GCTTACGCGG GCAGTTCGGC GAGCGCTCG GCGGTCAGCG CGTTAGCAC GCCCGCGCAG 840
ATGCGCAACC CGACCGCTCA GGTACGCA GCGCGCGCGG TGCCACCGCG CGCCGCTACC 900
GCCAGTCCGA CGTGACCGA GATGATCACC GCGCTACCCA ACCGCTGCA AAGCCTCACC 960
TCACATCTGT TCGATGCTG TAACGGTCGG CTGTGCTGGC TGTGGCAGAT CTTGTTGGGC 1020
ACGCCCCATT TCCCACTC ATTTCGGA CTCCTGACCG ACCTGCAGCC CTACGGGAGC 1080
TTTNTNTATA ACACCGAGGG CTTGCGGTAC TTCAGCATCG GATGGGCAA CAACCTCAAT 1140
CAGTCGCCCC AGACCTTGGG ATTGATCGGC TAGGCGGCAC CGCTTCGGCT CGCGGCTGCT 1200
GGGATGCGG CCAAGGCTT GCTTGACTG GCGGGGATGC TGGTGCGCGG GCGGCTGCG 1260
GCGGCTCTGG GCAATCGCGG TTCGGTTGG AACCTGTGG TGGCGCGGT GTGGANTGGA 1320
CCTTGGCCCG GTTCGGTGAC TCCGGGGGCT GTCGCGTAC CGGTGACTAC GGTCAATGCC 1380
GCCCCGAGGG CGCGCCCGG AAGCCTGTT GCGGCGCTGC CGCTANCTGG TCGGGGCGGG 1440
GCGCGCGCGG GTCCACGCTA CCGATTCCCT CCCACGCTCA TGCTTCGCCC ACCCTTCGMC 1500
GGGATAGTGG CTGCGGCAAC GTATTAACGG GCGCGGCTCG GCTGCTGTGG TCGGCTGCGG 1560
GTGGCAATTG GTGCGCGCGG AAATCTCSGT GGGTTATTTT CGGTGGGATF TTTTCCCGAA 1620
GCGCGGTTCA RCACCGGATF TCCTAACGGT CCGCKACTC TCGTGGCGAA TTCGGCCTCA 1680
AGTGACGTCC GCGGAAACCG CTTGGGTTT GAAAGCTTCA GAAAGGCCCC CTCGAGGGGG 1740
TTCGGCAAA C GG 1752

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(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```

Met Asp Phe Gly Ala Leu Pro Pro Glu Val Asn Ser Val Arg Met Tyr
 1          5          10          15
Ala Gly Pro Gly Ser Ala Pro Met Val Ala Ala Ala Ser Ala Trp Asn
 20          25          30
Gly Leu Ala Ala Glu Leu Ser Ser Ala Ala Thr Gly Tyr Glu Thr Val
 35          40          45
Ile Thr Gln Leu Ser Ser Glu Gly Trp Leu Gly Pro Ala Ser Ala Ala
 50          55          60
Met Ala Glu Ala Val Ala Pro Tyr Val Ala Trp Met Ser Ala Ala Ala
 65          70          75          80
Ala Gln Ala Glu Gln Ala Ala Thr Gln Ala Arg Ala Ala Ala Ala Ala
 85          90          95
Phe Glu Ala Ala Phe Ala Ala Thr Val Pro Pro Pro Leu Ile Ala Ala
100          105          110
Asn Arg Ala Ser Leu Met Gln Leu Ile Ser Thr Asn Val Phe Gly Gln
115          120          125
Asn Thr Ser Ala Ile Ala Ala Ala Glu Ala Gln Tyr Gly Glu Met Trp
130          135          140
Ala Gln Asp Ser Ala Ala Met Tyr Ala Tyr Ala Gly Ser Ser Ala Ser
145          150          155          160
Ala Ser Ala Val Thr Pro Phe Ser Thr Pro Pro Gln Ile Ala Asn Pro
165          170          175
Thr Ala Gln Gly Thr Gln Ala Ala Ala Val Ala Thr Ala Ala Gly Thr
180          185          190
Ala Gln Ser Thr Leu Thr Glu Met Ile Thr Gly Leu Pro Asn Ala Leu
195          200          205
Gln Ser Leu Thr Ser Xaa Leu Leu Gln Ser Ser Asn Gly Pro Leu Ser
210          215          220
Trp Leu Trp Gln Ile Leu Phe Gly Thr Pro Asn Phe Pro Thr Ser Ile
225          230          235          240
Ser Ala Leu Leu Thr Asp Leu Gln Pro Tyr Ala Ser Xaa Xaa Tyr Asn
245          250          255
Thr Glu Gly Leu Pro Tyr Phe Ser Ile Gly Met Gly Asn Asn Phe Ile
260          265          270
Gln Ser Ala Lys Thr Leu Gly Leu Ile Gly Ser Ala Ala Pro Ala Ala
275          280          285
Val Ala Ala Ala Gly Asp Ala Ala Lys Gly Leu Pro Gly Leu Gly Gly
290          295          300
Met Leu Gly Gly Gly Pro Val Ala Ala Gly Leu Gly Asn Ala Ala Ser
305          310          315          320
Val Gly Lys Leu Ser Val Pro Pro Val Trp Xaa Gly Pro Leu Pro Gly
325          330          335
Ser Val Thr Pro Gly Ala Ala Pro Leu Pro Val Ser Thr Val Ser Ala

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	340		345		350										
Ala	Pro	Glu	Ala	Ala	Pro	Gly	Ser	Leu	Leu	Gly	Gly	Leu	Pro	Leu	Xaa
	355		360		365										
Gly	Ala	Gly	Gly	Ala	Gly	Ala	Gly	Pro	Arg	Tyr	Gly	Phe	Xaa	Pro	Thr
	370		375		380										
Val	Met	Ala	Arg	Pro	Pro	Phe	Xaa	Gly	Ile	Val	Ala	Ala	Ala	Thr	Tyr
	385		390		395										400

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GCCACGAGCA	CCAGTTGACC	CCGGAAGAAC	CTACCCGCGC	CACCCAGGCG	CGCCCCGATC	60
ACCGGCCCGG	TCCACCAAC	CTTTTCGGTA	AACGAGCCAC	TCCAGCGGAG	ATCGGTACCG	120
CCCGACGCAT	TTGGTSTAAG	GACCACCTCG	CCGAGTAGT	CCTGGACGGG	TGTCTCGCG	180
CCACCCAGCT	TGTAGACGTG	GCGACGGTCC	TGCTCATACT	CGACGGTCTC	TTCCTGCACG	240
AACACCGGCG	ACATGCGTAG	TTTCGGGATG	GCCCCGATGC	CGCCGGGCGC	CGGATCACCG	300
CCTCGCGGCC	AATCGATTG	AGCAACGATG	GGCTTGGCCC	AGGTGCCCCA	GTTGCCACCG	360
TCTGTACGSA	GCCGAACAA	GTTTGCAGCC	GGCGCGCTGC	TGGTCTTGST	GACCTCGAAC	420
GAAATTTTCC	GACCCGACAT	GCGGACTTCC	CGAAACGACA	ACTGAAGCTC	GTGC	474

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

CTGGCGCGCG	GAAAAAANTA	TTACTGGCAG	GACCGGCAGA	ATCATGCGTG	ATATTCCGGT	60
GATGAGGCGG	CCGAGGAACC	GACTAGTGC	AGGGTCAACA	CATCGGTTAT	TGTTGCGGT	120
TTAGGTCTTG	GATCTGCGG	GACGGCAACG	AGTTGGCAGG	ACCGCTCAGG	CGAGCGCTGT	180
TGACAGAGTC	GCTTCACGTC	GAATCGGCGA	CCGCTCAGAT	GCGAATGATA	GCCACATCGG	240
CCACACGCTC	GACGGCGCTG	AAGTCGCGGT	CGTGGGTGAC	GACCGGCACC	CCTTGGGACG	300
TGGCAACGGC	AGCGGCGCTC	ACCGGACGGG	ACCGAGATCG	TGGGTGCTGT	CGCCAGTBA	360
CGTTGCGAGG	TGCGGGGTGC	AATCCCGCAT	CTGCTTGCCT	ATGCGGAAGC	CGCCGAGCA	420
GCTCGCTCTG	ACTCAACCAT	CGGCGCGCTG	CGGGCTGCTT	GCGGTGAGCA	GCGCAACGGG	480
TTTGGCGTTC	GCAGTGATGG	TGATGTCCTC	GCGGGCGTGC	ACGCGCCGTA	GCAGCCCGGC	540
GGTGTGTGTC	CGCAGTTGCG	GAGACGCGAC	TTGAGCAGGC	ATGCTGCGGG	GATCGGCTTG	600
CGCTGGGCGC	GGTGTACCG	TGATGCGCTT	GGGATATCAC	GTGATCTATC	GCCACGAAGC	660
CGCGGATGA	GCGAGGCAA	CGGCTACAC	GGGCTGCGTC	GCGTTGACCG	CGCGGAACGT	720
TACTGTGCGG	GGGGCATCAG	CACCGTATCG	ATCATGTACA	CCGTGCGCTG	GCGGTGTGA	780
CTCGGCGACA	TACCAACCGG	GCTGTGTGA	CGATGAGTGC	TGCGGGGCGC	CTATCACCGT	840

CAGGTCGGCA	CCTTCCAGGT	CTGATGGGTG	CCGTCCGATCC	TGCTCCGACT	CGCCTGGGCC	900
GCTATCACGT	GCTAGGTCAG	GATGCTGCTG	AGCAGCTTGG	CGTCAGTCTT	GAGTTGATCG	960
ATAGTGGCCG	CGGCGAGCTT	GTGGAATGCG	GGCTTGGTGG	GGGCGAAAC	GGTGTACTCG	1020
CCGCCGTTGA	GGGTGTCGAC	CAGATTACAC	TCCGGGTTCA	GCTTCCCGGA	CAGAGCCGAG	1080
GTCAAGGTTAC	TGAGCATCGG	GTGTGTTGAA	GCCGCGGTAG	CGACCGGGTC	TTGCGCCATT	1140
CCGCCCAACG	ATCCGGGACC	GGTGGGATTT	TGCTCCGCGT	ATTGCGCGCA	CCCACGACCA	1200
ATCAGGTCCG	CTGCGGTCAG	CCATTGCCGC	CGTGTTAACG	GGCGCCGCGG	GGCTGGTCGC	1260
CGGTTTCGGG	CTGGTGTCTT	GCGACACGGG	TTTGGTGTCT	GAACAACCGG	CTAAGAAGCG	1320
AATCGGATG	GCTCCGAGGC	TGCTGCTGCG	GGCCGGTTTG	GCTTGAACGT	TGATCATGCG	1380
TTGATTCTCT	TTGCTTCTGC	GGCGGGGTTG	AACGCCGTCC	TCTTGGGTGG	A	1440

(3) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGAGAGT	CGTATCTTTG	CACCCAGCGC	CCGTAGGAAA	CCGCTGGGCT	GGCTAACTCA	60
GAATCGGGCG	GCCGTCGATT	CGAGAGGTAA	CCGATCGGCC	GCCGACAATG	GGTTACCCAC	120
CGAGACTGAT	TGCGCGCAG	CCGCTTGG	CGTCTAAGCG	CCGTTTCGTG	CATGCCCGGA	180
ACGGCTGCAC	TACCGACCT	TCTACGTAGT	ACGTGACCGA	CTTTTACCGA	TTATCGCTGA	240
CGATCTTTGC	CTCCAGGAC	TCCAGATCT	ACTCGTGCC			279

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

ACCGCCACCC	GCAGCCCGGA	ATCACCGTCG	GTAACCTGCC	AATACAATTT	CTTCATCGAC	60
GACTTCGGGA	ACAGCGAACC	CGAGCCCAAC	GCCTGATAGC	CTTCTTCCTC	GATGTTCCAA	120
CCGCCGGCGG	CGTCGAACGA	AACGATACGA	CCCGCGCTCT	GCAGGTCAGA	CGCATGAATG	180
TGCTAGCCCG	CCAGCAACCG	CAACGCCGAC	AGACCTTGCA	TCCCGGCTCC	CAGATTGCCA	240
CGCACCATAA	TGCGCAGCGG	GTTGATTTTG	CCGCGAAACG	TCAGCGGCAC	ACCTTCGAGC	300
TTCTCGTAGT	GCTCAAGTTC	CACGGCATA	AGCCGGGCAA	ACTCAACCGC	GACCGCAGCC	360
GTGCCAGCGA	TGCCGTAGC	GGTGTAGTCA	TGCTGATAT	ACACCTTGCG	CACATCACCC	420
CCAGAAATCA	TGTTCGCTG	CGTCGAACCG	CGGTACCCCG	CCATGACAAC	ACCGCGGGGG	480
TATTTACGGG	CGACAATGGT	GGTGGCGTGC	GGCAGTTGCG	CATCGCCGCG	TGCGAGTGGC	540
GACCGCCCGC	TGATGCTTGC	CGGCAGCAAC	TCCGCGGCGT	GGCGCGGCAG	GAAGTCAAGT	600
GAAAGAAGAT	AGGTCTACAG	CGGCTGTTTC	AGAGAGTGAA	TTAATGGACA	GGCGATCCCG	660
CAACCGCCAG	GTCACTGTCC	GCCCTTTTGG	ACGTATGCGC	GGACGAAGTC	CTCGGCGFTC	720
TCTTCGAGGA	CTTGGTCGAT	TTCTTCGAGC	AGATCGTCCG	TCTCTCGGCT	CAGCTTTTGG	780
CGACGCTCCT	GGCCCGCGGC	GGTCTGCGCG	GGGATGTCGT	CATCATCGCC	GCAGCCACCG	840

```

CCACGCTTGG TCTGCTCTTG CGCCATCGCC GCGTCTGCTT TCTCATGGC CTTTCAAAAG 900
GCCGCGGGTG CCGCTCACAC GCGCGCTGTC TTCTCTTCAC CTACCGGTCA ACACCAACGT 960
TTCCCGGCTT AACCAGGCTT AGCGAGGCTC AGCGGTCACT TCTCTACCA GCTCCACGGC 1020
ACTGTCCACC GAATCCAGCA ACGCACCAAC ATGCGCTTCA CTACCCCGCA ACGGCTCCAG 1080
CGTCGGGATG CGAACCAGCG AGTCGCGCGC AGSTCGAAGA TCACCGAGTC CCGCTAGCC 1140
CGCGCGATAT CAGCCCCGAA CCGCGCGAGG CATTTGCGCG CGGAATACG CCGGGGTGTC 1200
GGTCGCGCGT TCTCCACGGC ACTCAGCAGC TGGTGTTCG GTGACTAAAC GCTTATGGA 1260
GCCGCGCGCG ACCAGCGCGT TGTACAGGCC CTTGCTCCAG CGGACATCGG AGTACTGCAG 1320
GTTGACGAGG TGCAGCCCGG GCGCGGACCA GCTCAGGTTT TCCGCTGCC GGAACCGCTC 1380
GAGCAGCGCG ACTTTGCGCG GCCAGTCCAG CAGCTCGCGT CAATCCATCG GGTCAACGCTC 1440
GAGCTGATCC AGCACGTGTG CCCAGGTTTC

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

ATTCCCATCG CTCGGGCLCC TATCACCAGG TAGTCGGTTT CGATGGTTTT CGCGCGCCCT 60
TGCCTTGGCC TGGGCGACCG GTGCTTCATG GCGCCTCTTG TCGGATTGG AATTTGTGAC 120
AACGAAATCG GCGCATCGGT GAGCAATCGT CGCCGATGCA AGACACGCTT TCGCTGCGCG 180
GGCGTCAGGT GGAGTTTAGG CCGCCGTAA CAGGTAGACC GCGCACTGAC CAACCCCAA 240
ACCCACAAAC CCTGGACGCA TCGGGTCTC GGGCTTCAA TTCCGGGTAG ATATCGTATA 300
CGGATATCGG ATGCCGTAGC CTTATCGAGG CATGAGACCG CCGCTAGACC CACCGGATAT 360
TCCAGATGAG CTCGCGCGAC GCTTGGGCT CTGGATGCG GTGGTGATCG GGCTTGGGTC 420
CATGATCGGT GCGGGAATCT TTGCTCGTGC CGAATTCGGC ACGAGCTCGT GCGGAATTCG 480
GCACGAGATT CCAATCCCCA GAAGGTCTG CAGGCGTCA ATGCGACTTG ATCGTTGAT 540
CGATGATGAA CGCTCTGCTC ATGCGTGGCG CCTATCTCAA CGGTCTGCGA TTCCATGCA 600
TAGCCTTGGT TCTGCATTGC ACGCGTAGGG CTTACAGTCT GGCTGTGATG CTTGGGCGAT 660
GTCAACAGTT TTTTTCATGC TAAGCAGATC GTCAGTTTGG AGTTCTGAA GACGGCATGT 720
TCACTTGTTG TCGACTACAT CGTCTGCGCA CATTTGCCCT CCGCAACTG CGCTGCGACA 780
ATGCGCCAA CCGCTGTAG CTGTCGCGCA ATTGGGACG AGGATCCACC GGAGATGGCC 840
GACGACTAGC ACGAGGCGTG GATGCTCAAC ACCGTGTTTG ACTATCACA CAGGACCGCA 900
AAAGAAGAGG TCATCCATCT CGTGCCCGAC GTGAACAAGG ACAGGGGGCC CATCGAATC 960
GTAACCAAGG TAGACAAAGA GGGACATCAG ACTGCTCTAC GATCGGGAGC CACGTTTTC 1020
TACAAGGAAC ATCTAAGTT TTGATTCGGG AACATCTA

```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```

GCACGAGGCA TTGGCGGGCA TCTGCATAAA CGGTGACGTA TCAGCACAAG ACAGCGGAGA      60
GAACAACATG CGATCAGAAE GTTCCGGTGG GCTGXTAGCC GCAGAAAGTC COTTCCGCTC      120
GGTGTATTTC GACGACTGCG ACGACTCGTG CCG                                     153

```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```

CCGCGCGGCTC GATCAGCGAG CCAAGCAAAA ACTCCGTGGA GCCCGAGTGG ATGATGGTCA      60
CCCGCGCGCAG CATCTGGCGA ACGATCACCT CGATGTGCTT GTCTGGATC GACACACCTT      120
GGCGCGGCTTA GACCTGCTGG ACCGCCGAA CCAGGTGTAT CTGCACCTCG CCGGGGCCCCT      180
GCACCGCGAG CACCTCATGC GGGTGGGCGG AGCTTTCAT CAGCTGCTGG CCCACCTCGA      240
CGTGGTCCGC ATCGGAGAGC ACCCGTTGG AACCTTTTC GTGCTTGAA ACCCGCAGCC      300
GCTGGCGCTT GGAGATCTTG TCTAGACCA CTTCCTCACC GCCGTCTCA GGAACGATGG      360
TGATGTTGTA GAACCGCTCG CCGTCCT

```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```

GTTCAAGCAG GCTATCCGAT TGTCCGCTC GCTTCGGTGG GTCTGAACA CGGCATCGAC      60
ATCGTGCTCG ACAACGAATC CCGACTGCTG GCACCGTTCC AGTTCTTCC CGAGAAGCTG      120
CTCGGCGACA AAGACGGTCC GCGCTGGTTC CGTGGTGGCG GACTGACACC GGTACCGCGC      180
CCCGAAGCGC AGTATTACTG GTTCGCGGAG CCAACCGACA CCACAGATT TATGGGUCAG      240
CAAGCCGACG ATAACCGGCG ACGCAGGGTG CCGAGCGCTG CCGCGCGCGC TATCGAACAC      300
GGCATCGAGC TGATGCTGGC CGACCGCGCA GCGATCCCA ATCGATCCCT GGTCCGACGG      360
CTCTTGGCTT CCGACGCTTA AGCGCGCCC

```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```

CCCGCCGTCG GAATGATCCC CGTCTCGTCG CCGCCCCATT TGATGCTGTT GATGAGCTGT 60
TTGGAGAAAC CCGGTTGGCG TACCGGTGAG CCGGAATATC TGTTCGAAGC GTACCCGAT 120
GTACACATGA ANTNCNTTGN CCGGTGNGCG GTNTTGGNTG NCGNAAACAC GTGTTGNTA 180
AGCCTTGNTG GNTCTGNAAG NGCCGTNGAC GCCTGTGTTC CCGAAGATAA TGAGCACCTG 240
ACCGTTGCGC GATCGCCCTT TATCCCAAGG AATTCCGAGG TCGGTCCCGG AGATGCCGAA 300
GCGTTCAGG GTCCTGTGCG GCGTGTCCCG TCCGTTCACC CACTCGGCCA GGGATGTGGN 360
AGCCCGGCGG AGCGTGGCAC CAGGATCCCG CCGCGCCGCC GGAGCAGGGT CGGNNCTGN 420
NCTGNTTTC TNNGCCNAA TTNNACTCN NCAACANCT TGNNGCGAC TCNNACCGN 480

```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```

GCACGAGGCT ACCGGCGCGT CCGCCGCCAT GCGGTGGATG CACGCGTAGC CACCCGTNCA 60
TNCAGCGGCT CAGCGCGCGC GTCCGGGCTT AACGUTATAG CAGCTGCAAA CACCCAGCG 120
CCGGCAATTA CTTTGATGTT GAACCATGA CUATNGCTTN CGNTNCAAT CTCNTCTCTT 180
NCGCGCGCNC TATTNNNGCC ATAMATTTCG TTNNANNCGN AACGCTAGAC GTATCGASTT 240
CCTTTTCGAC CACCGGCTCA ATGTTCAGCA TCCTATGGGG AACATGAGCC CCGCCGCRCC 300
GGGCGGTTTC CALATGGTGA CFTCACAACG GTGTCAACAG CUAGCGCAAT GTCCGCGTA 360
GGGACCGGCG GCGTGGGATC GGTGGGGTGA GCGCCCGGCT TCTCAAAGCG AGGGGAGCCC 420
CGGGACTCTT ACCGGCCGAA GCGGCGGGT GTCACTGATC TAGGCTGACG GCCAGTGGTT 480
GNTNAGCCAA CAAGGATGAC NACAAATAAN CCGAGGAGAG ACANNGAGCG GNGCGAHANG 540
CTNANCCGNN HTTGNNCNA NNNMACNAC TTNTACGNN CTTATGN 587

```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```

CAGGCATGAG CAGAGCGTTC ATCATGATC CAACGATCAG TGCCATTGAC GCCTTGTACG 60
ACCTTCTGCG GATTGGAATA CCGAACCAAG GGGGTATCCY TTACTCTCTA CTAGAGTACT 120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCGCGG TGATGGCTCG TTAGGTTCG 180
CCGCGGACAA ATACGCGCGC AAAAACCACA ACCAGTGAA TTTTTCAG GAAGTGGCAG 240
ACCTGATGCG TCACTCATC AGCCTGATCC ACGACAGGC CAACGCGGTC CAGACGACCC 300
GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTGCT GCGCCCGGTG GCTGTGACCC 360
TGACCTACAT CCGGTCCTC GGGCACGCC TATCGGCGCC CTTCCAGGCG CGGTTTTCG 420
CGGGCGCAT GCGCGTACTG GCGGCGCGC TTGCTTACTT GGTGCTGAAA ACGCTGATCA 480
ACCGACTCA ACTCTCAA TTGCTTSCCA AATTGGCGGA GFTGGTGGCG GCGGCCATTG 540
CGGACATCAT TCGGATGTG GCGGACTCA TCAAGGCGAC CCGCGAGAA GTGTGCGAGT 600

```

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```

TCATCACAAA CCGCCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACC GGGTGGGTGA 660
CCGGACTGTT CTCTCGAGGG TGGTUGAACC TGGAGTCTCT CTTTGGGGGC GTCTCTGGCT 720
TGACCGGGGC GACCACGGGC TTGTGGCAAG TGACTGGCTT GTTCGGTGGC GCGGTCTGT 780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGGAG CTCAGCCAGC TTGCCCCCCC 840
TGGCCGGCAT TGGGGGGGGG TCGGTTTTG GGGGCTTGGC GAGCCTGGCT CAGGTCCATG 900
CCGCTCAAC TCGGAGGGC CTACGGCCCC GAGCTGATGG CCGGTCGGC GCGGTGGC 960
AGCAGGTGG CCGGCACTG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGCGGAC 1020
CGTAGGCAT GGGCGGCATG CACCCCTCTT CCGGGGGCTC GAAAGGGACG ACGACGAAGA 1080
AGTACTTGA AGCCCGGGC GCGGCACTG AAGACGCCGA GCGCGGCCA GTCGAAGCTG 1140
ACCGGGGGG TGGCCAAAAG GTGCTGCTAC GAAACGTCT CTAACGGCAT GCGGAGCCAA 1200

```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
1      5      10      15
Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
20     25     30
Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Ala Leu Glu Glu Leu Ala Ala
35     40     45
Ala Phe Pro Gly Asp Gly Trp Leu Gly Ser Ala Ala Asp Lys Tyr Ala
50     55     60
Gly Lys Asn Arg Asn His Val Asn Phe Phe Gln Glu Leu Ala Asp Leu
65     70     75     80
Asp Arg Gln Leu Ile Ser Leu Ile His Asp Gln Ala Asn Ala Val Gln
85     90     95
Thr Thr Arg Asp Ile Leu Glu Gly Ala Lys Lys Gly Leu Glu Phe Val
100    105    110
Arg Pro Val Ala Val Asp Leu Thr Tyr Ile Pro Val Val Gly His Ala
115    120    125
Leu Ser Ala Ala Phe Gln Ala Pro Phe Cys Ala Gly Ala Met Ala Val
130    135    140
Val Gly Gly Ala Leu Ala Tyr Leu Val Val Lys Thr Leu Ile Asn Ala
145    150    155    160
Thr Gln Leu Leu Lys Leu Leu Ala Lys Leu Ala Glu Leu Val Ala Ala
165    170    175
Ala Ile Ala Asp Ile Ile Ser Asp Val Ala Asp Ile Ile Lys Gly Thr
180    185    190
Leu Gly Glu Val Trp Glu Phe Ile Thr Asn Ala Leu Asn Gly Leu Lys
195    200    205
Glu Leu Trp Asp Lys Leu Thr Gly Trp Val Thr Gly Leu Phe Ser Arg
210    215    220
Gly Trp Ser Asn Leu Glu Ser Phe Phe Ala Gly Val Pro Gly Leu Thr
225    230    235    240
Gly Ala Thr Ser Gly Leu Ser Gln Val Thr Gly Leu Phe Gly Ala Ala
245    250    255

```



```

Gly Leu Ser Ala Ser Ser Gly Leu Ala His Ala Asp Ser Leu Ala Ser
      260      265      270
Ser Ala Ser Leu Pro Ala Leu Ala Gly Ile Gly Gly Gly Ser Gly Phe
      275      280      285
Gly Gly Leu Pro Ser Leu Ala Gln Val His Ala Ala Ser Thr Arg Gln
      290      295      300
Ala Leu Arg Pro Arg Ala Asp Gly Pro Val Gly Ala Ala Ala Gln Gln
      305      310      315      320
Val Gly Gly Gln Ser Gln Leu Val Ser Ala Gln Gly Ser Gln Gly Met
      325      330      335
Gly Gly Pro Val Gly Met Gly Gly Met His Pro Ser Ser Gly Ala Ser
      340      345      350
Lys Gly Thr Thr Thr Lys Lys Tyr Ser Gln Gly Ala Ala Ala Gly Thr
      355      360      365
Glu Asp Ala Gln Arg Ala Pro Val Gln Ala Asp Ala Gly Gly Gly Gln
      370      375      380
Lys Val Leu Val Arg Asn Val Val
      385      390

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

ACGTTTACCC ATGCCGTCGG TCCAGAGCAA CGCCAGACAA CACAAAGTAG TCTAATTCCG      60
TTATAAAGCA GACATTTCCG TGTTATGTA GAAGATGTGG ACCGATCAGA TGAAGCGATC      120
CGGTCAGGT GGTATCCGAT GTCTTTGTG ACCATCCAGC CGGTGCTCTT GGCAGCCGCG      180
ACGGGGGACT TCCGACGAT CGGTACCGCC GTGAGTGTCT GGAACACAGC CGTCTGTGCC      240
CCGACGACGG GGTGTATTAC CCTGCTGCC AATGACGTGT CGGTCTTGAC GGGGGGCCGG      300
TTCACCGCGC ACACCAAGCA CTACCGAGTG GTGAGTAAGC CCGCCGCGCT GTTCATGCGC      360
ATGTTCTGGG CCTTCCCGGC GGGCACCGCC GATCGGTATG CGACCACCGA GGCTGTCAAT      420
GTGCTCGCGA CCGGTTAAG

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

GAGGTTGCTG GCAATGGATT TCGGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA      60
TTCCGGTCCG GGGCCGGAGT CGATGCTAGC CCGCGCGGCC GCGTGGGACG GTGTGCCCCG      120
GGAGTTGACT TCCGCGCGCG TCTCGTATCG ATCGGTGCTG TCGACGCTGA TCGTTGAGCC      180

```

```

GTGGATGCGG CCGGCGGCGG CCGGATGCGG GGGCGGCGCA ACCCGGATG TGGGGTGGCT 340
GGCCGCCAGG GCGGCGCTGG CGAAGGAGAC GGGCACACAG CCGAAGGCCAG CCGGCGGAGC 350
GTTTGGGAGG GCGTTCGCGA TGACGGTGCC ACCATCCCTC GTGCGCGGCA ACCCGAGCCG 360
GTTGATGTGG CTGGTCGCGG CGAACATTCT GGGGCAAAAC AGTGGCGGCGA TCGCGGCTAC 420
CTAGGCGGAG TATGCCGAAA TGTGGGCGCA AGACGCTGCC GTGATGTACA GGTATGAGGG 480
GGCATCTGGG GCGGCGTTCG CCTTGCCTGC GTTCACTCCA CCGGTGCAAG GCACCGGCCC 540
GGCGGGGGCC GCGGCGGCGG CCGCGGCGAC CCAAGCGGCC GGTGCGGGCG CCGTTCGCGA 600
TGCACAGGCG ACACTGGGCG AGCTGCCCCC GGGGATCTCG AGCGACATTC TGTCCGCTAT 660
GGCGGCCAAG GCTGATCGCG TGACATCGGG ACTGTTGGGG ATCGCGTCTG CCGTCAACCC 720
GCGAGTCGGA TCCCTCAGC CGATAGTGAT CCGGACCCCG ATAGGGGAAT TGGAGCTGAT 780
CGCGCTCTAC ATTGCATCCA TGCGACCGCG CAGCATTCGG CTGCGGATCA CGAACACGCG 840
CAGACCTCTG CACATCGGGC TATACGGGAA CGCGGCGGGG CTGGGACCGA CGCAGGGCCA 900
TCCACTGAGT TCGGCGACCG ACAGGCGGGA GCGGCACTGG GCGCCCTTCG GGGGCGGCGC 960
GCGGCTGTCC GCGGCGCTCG GCCACGCGAG ATTAGTCGGA GCGTTGTCTG TCGCGCACAG 1020
CTGAGGACCG GCGGCGGCGG AGATCCAGCT CGCGCTTCAG GCAACACCCA CTTTCAGCTC 1080
CAGCGCGGCG GCGGACCGGA CGGCTTAAA CGGGATGCGG GCAGGCGCTG TCAGCGGGAT 1140
GGCTTTGGCG AGCGTGGCGG CAGCGCGGCG GAGGCGCGGT GCGGCGACCG GTAGCGGCGC 1200
CAGCACTGAC GCGCAAGAGG AGGCGCGGCA ACCCGCGGTA GTTGTGATTA GAGAGCGAGC 1260
GCGGCGGCGA AACCGCGGCG GGTAAAGTCC CGGCAACCGT TCGTGGCGCG GCGGAAATG 1320
CCTGCTGAGC GTGCTATCC GACGCGCGGT TCACACCGCT TGTAGTAGCG TACGCTATG 1380
GACGAGGCTG TCTGGATTCT CGGCGGCTAT CAGAGCGGAT TTGCTCGCAA CCTCGGCGAA 1440
G 1441

```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

Met Ser Phe Val Thr Ile Gln Pro Val Val Leu Ala Ala Ala Thr Gly
 1              5              10              15
Asp Leu Pro Thr Ile Gly Thr Ala Val Ser Ala Arg Asn Thr Ala Val
 20              25              30
Cys Ala Pro Thr Thr Gly Val Leu Pro Pro Ala Ala Asn Asp Val Ser
 35              40              45
Val Leu Thr Ala Ala Arg Phe Thr Ala His Thr Lys His Tyr Arg Val
 50              55              60
Val Ser Lys Pro Ala Ala Leu Val His Gly Met Phe Val Ala Leu Pro
 65              70              75              80
Ala Ala Thr Ala Asp Ala Tyr Ala Thr Thr Gln Ala Val Asn Val Val
 85              90              95
Ala Thr Gly

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid

91

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Asp Phe Gly Leu Leu Pro Pro Glu Val Asn Ser Ser Arg Met Tyr
 1           5           10           15
Ser Gly Pro Gly Pro Glu Ser Met Leu Ala Ala Ala Ala Ala Trp Asp
      20           25           30
Gly Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val
      35           40           45
Val Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala
      50           55           60
Met Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala
      65           70           75           80
Ala Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala
      85           90           95
Phe Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala
      100          105          110
Asn Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln
      115          120          125
Asn Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp
      130          135          140
Ala Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala
      145          150          155          160
Ala Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro
      165          170          175
Ala Gly Pro Ala Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly
      180          185          190
Ala Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile
      195          200          205
Leu Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr
      210          215          220
Ser Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser
      225          230          235          240
Ala Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile
      245          250          255
Ala Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile
      260          265          270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
      275          280          285
Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
      290          295          300
Pro Gln Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
      305          310          315          320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
      325          330          335
Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
      340          345          350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
      355          360          365
Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
      370          375          380

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Gly Thr Thr Gly Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385                390                395                400
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
405                410                415
Pro Pro Gly Asn Pro Pro Arg
420

```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

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Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1                5                10                15
Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
20                25                30
Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
35                40                45
Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
50                55                60
Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
65                70                75                80
Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly
85                90                95
Phe

```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

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Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Ala
 1                5                10                15
Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg
20                25                30
Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xaa Val Ser
35                40                45
Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln Ile Tyr Gln Ala
50                55                60
Val Ser Ala Gln Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu

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65              70              75              80
Gln Xaa Xaa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Asn Ala Ala
      85              90              95
Ala Ala Gly

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Claims

1. A polypeptide comprising an antigenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 1, 11, 12, 83, 103-108, 125, 127, 129-137, 139 and 140 or a complement thereof under moderately stringent conditions.

2. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 16-33, 109, 126, 138, 141, 142 and variants thereof.

3. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.

4. A recombinant expression vector comprising a DNA molecule according to claim 3.

5. A host cell transformed with an expression vector according to claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.

7. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with at least one polypeptide according to any one of claims 1 and 2; and

(b) detecting in the sample the presence of antibodies that bind to the polypeptide, thereby detecting *M. tuberculosis* infection in the biological sample.

8. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting a biological sample with at least one polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample the presence of antibodies that bind to the polypeptide, thereby detecting *M. tuberculosis* infection in the biological sample.

9. The method of any one of claims 7 and 8 wherein the polypeptide(s) are bound to a solid support.

10. The method of claim 9 wherein the solid support comprises nitrocellulose, latex or a plastic material.

11. The method of any one of claims 7 and 8 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

12. The method of claim 11 wherein the biological sample is whole blood or serum.

13. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA molecule according to claim 3; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

14. The method of claim 13, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA molecule according to claim 3.

15. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a DNA sequence that amplifies in the presence of the first and second oligonucleotide primers, thereby detecting *M. tuberculosis* infection.

16. The method of claim 15, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

17. The method of claims 13 or 15 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

18. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA molecule according to claim 3; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

19. The method of claim 18 wherein the probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 3.

20. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a DNA sequence that hybridizes to the oligonucleotide probe, thereby detecting *M. tuberculosis* infection.

21. The method of claim 20 wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

22. The method of claims 18 or 20 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

23. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide according to any one of claims 1 and 2; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

24. A method for detecting *M. tuberculosis* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and

(b) detecting in the sample a protein or polypeptide that binds to the binding agent, thereby detecting *M. tuberculosis* infection in the biological sample.

25. The method of any one of claims 23 and 24 wherein the binding agent is a monoclonal antibody.

26. The method of any one of claims 23 and 24 wherein the binding agent is a polyclonal antibody.

27. A diagnostic kit comprising:

- (a) one or more polypeptides according to any one of claims 1 and 2; and
- (b) a detection reagent.

28. A diagnostic kit comprising:

- (a) one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID NO: 2-10, 102, 128; and
- (b) a detection reagent.

29. The kit of any one of claims 27 and 28 wherein the polypeptide(s) are immobilized on a solid support.

30. The kit of any one of claims 27 and 28 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

31. The kit of claim 30 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

32. The kit of claim 30 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

33. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a DNA molecule according to claim 3.

34. A diagnostic kit according to claim 32, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA molecule according to claim 3.

35. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the primers being specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

36. A diagnostic kit according to claim 35, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotide of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

37. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA molecule according to claim 2.

38. A kit according to claim 37, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA molecule according to claim 3.

39. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

40. A kit according to claim 39, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a DNA sequence selected from the group consisting of SEQ ID NO: 2-10, 102, 128.

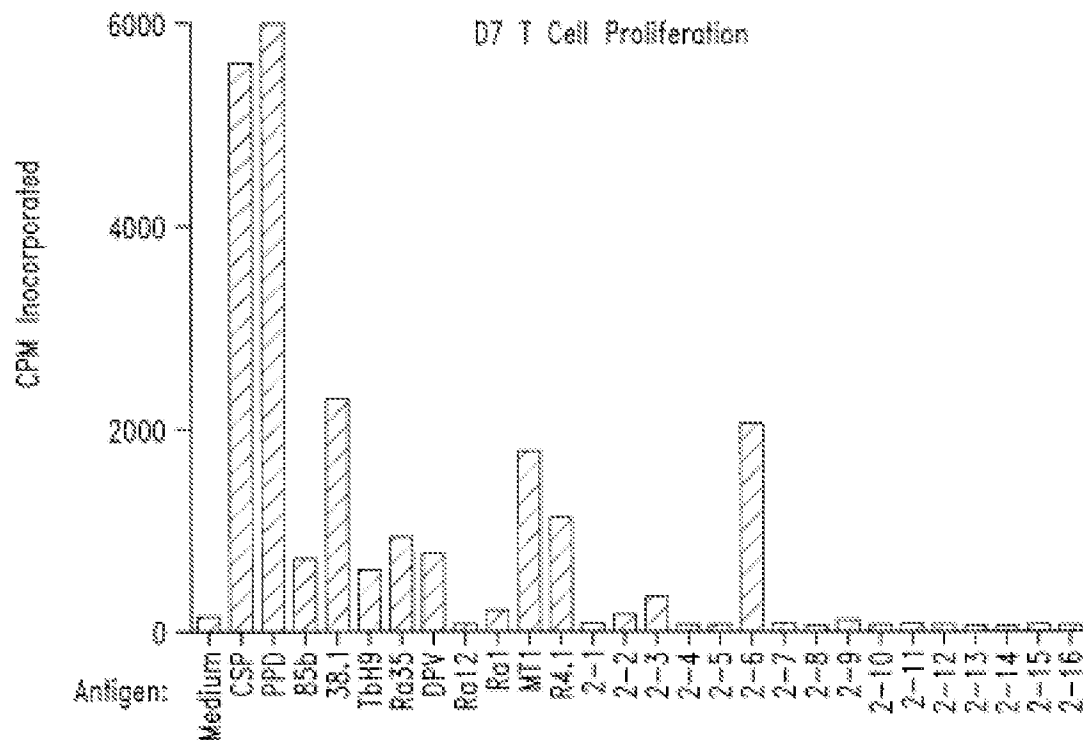
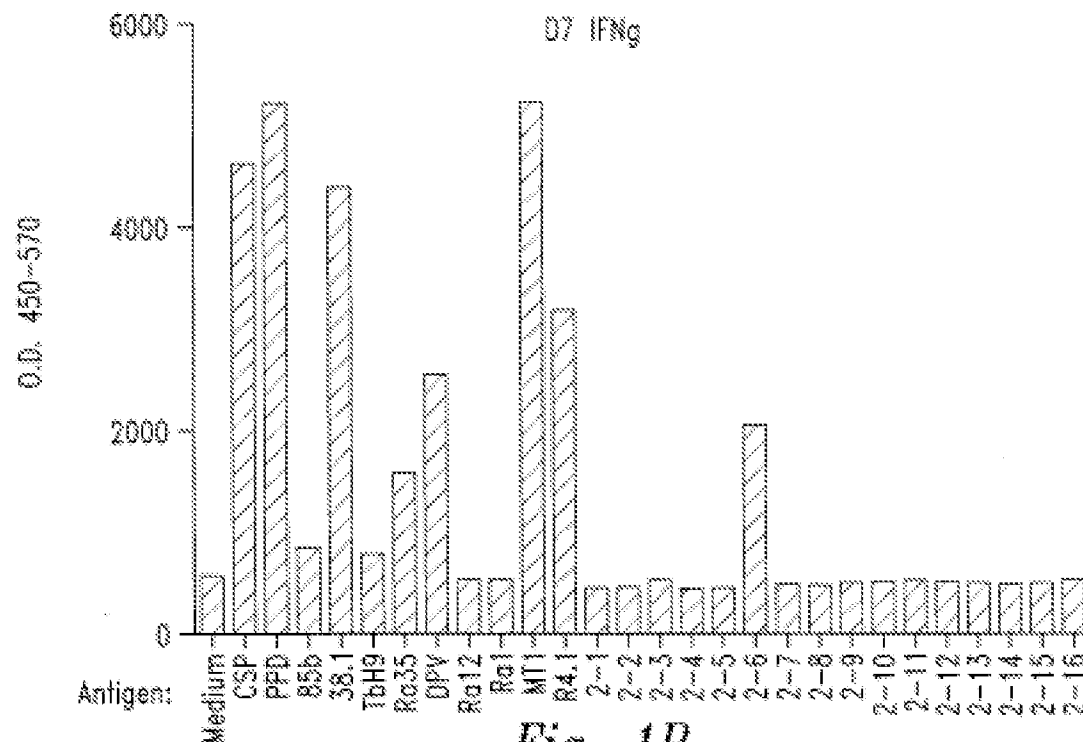
41. A monoclonal antibody that binds to a polypeptide according to any one of claims 1 and 2.

42. A polyclonal antibody that binds to a polypeptide according to any one of claims 1 and 2.

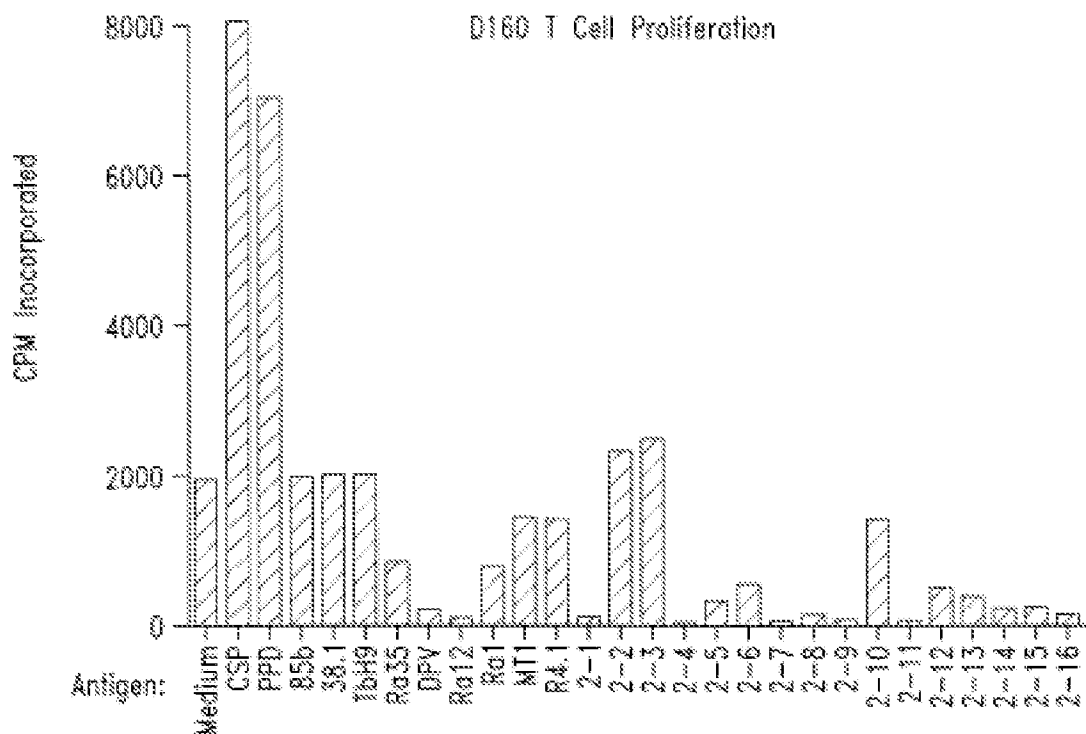
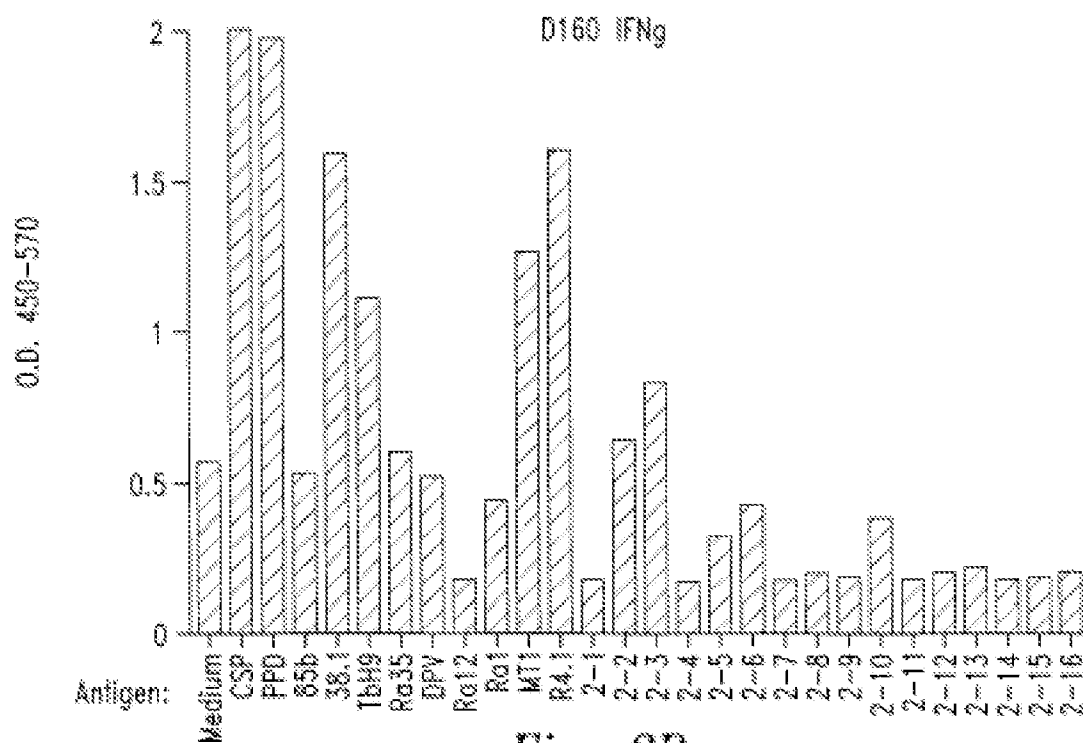
43. A fusion protein comprising at least two polypeptides according to any one of claims 1 and 2.

44. A fusion protein comprising at least one polypeptide according to claim 1 and a known *M. tuberculosis* antigen.

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*Fig. 1A**Fig. 1B*

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*Fig. 2A**Fig. 2B*